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Culicoides-borne diseases in the Indian Ocean: Examples of Bluetongue and Epizootic Hemorrhagic Disease fever viruses in Reunion Island

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ABSTRACT

Objectives: Bluetongue (BT) and epizootic hemorrhagic disease (EHD) viruses are two important vector-borne orbiviruses with a worldwide distribution that have major impacts on livestock breeding and trade. They are transmitted by hematophagous *Culicoides* species. If epidemiological investigations in epizootic territories conducted after massive outbreaks enabled to better understand the epidemiology of these diseases, their epidemiology remain poorly studied/understood in areas of endemicity. In this context, three studies were implemented in Reunion Island located in the South Western Indian Ocean

Materials and Methods: The three studies were: (i) a virological and serological survey on cattle to identify BT and EHD viruses seasonal dynamics and prevalence, (ii) an entomological study on *Culicoides* species diversity, seasonal dynamics and spatial distribution, (iii) a viral screening in *Culicoides* species to identify and better characterize the vector species involved in the viral transmission, the level of infection in field populations and virus dynamics in *Culicoides* populations.

Results: The period with highest levels of seroconversion occurred is the hot and rainy season, when incidence of antibody acquisition reached 36.7% (IC95% = [31.7%; 41.7%]) for EHD virus and 20.7% (IC95% = [16.3% ; 25.1%]) for BT virus. Five *Culicoides* species are described on the island, and seasonal dynamics is particularly marked for three of them. Four species are involved in the transmission of each virus.

Conclusion: Overall, BT is endemic with continuous virus circulation, limited clinical cases and high serological prevalence while EHD is epizootic with a marked seasonal transmission pattern.

Key words: Bluetongue, Epizootic hemorrhagic disease, *Culicoides*, epidemiology, Indian Ocean

A genomic map for bovine tuberculosis susceptibility in *Bos indicus* breeds

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ABSTRACT

Objective: This study aims to describe the genomic variation in bovine tuberculosis susceptibility within a *Bos indicus* population.

Materials and methods: A cross-sectional study of 2346 slaughter cattle was conducted in four regions of Cameroon. bTb was detected by culture in 150/162 animals with lesions. A subset of 239 cattle (culture positive and negatives) was genotyped using a BovineHD 777K BeadChip, their genomic diversity characterized and the admixture structure of the Cameroon cattle population estimated using principle component analysis (PCA), STRUCTURE, genetic relatedness and genetic differentiation (F_{ST}) analysis. Quantitative trait loci (QTL) which had previously been identified in *Bos taurus* was compared.

Results: We found that breed (within the *Bos indicus* subspecies) is an important factor in explaining the epidemiology of bTB, with Fulani breed appearing to be more susceptible then mixed breeds. The difference in susceptibly between *Bos indicus* subspecies could be due to their admixture structure. Therefore, selective breeding could be used to decrease the susceptibility of cattle to bTB which could reduce size and duration of outbreaks, providing a new viable option for targeted genetic disease control.

Key words: Cameroon, *Bos indicus,* bovine tuberculosis, admixture, susceptibility